

Best Local Similarity 100.0%; Pred. No. 3.9e-114;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLTLLFLTEALGDAAOEPTGNNNAEICLLPLDYGPCRALLLRYYDRYQS 60
DB 1 MDPARPLGSLTLLFLTEALGDAAOEPTGNNNAEICLLPLDYGPCRALLLRYYDRYQS 60
QY 61 CROFLYGCGEGNANNFYTWEACDDACWRIEKPVKYCRLOVSVDQCEGSTEKYPFNLSM 120
DB 61 CROFLYGCGEGNANNFYTWEACDDACWRIEKPVKYCRLOVSVDQCEGSTEKYPFNLSM 120
QY 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKIPSPFCYSPKDEGLCSANTVRYFNPXY 180
DB 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKIPSPFCYSPKDEGLCSANTVRYFNPXY 180
QY 181 RTCDAPFTYTGCGNDNNFVSRDECKRACAKALKKKKKMPKJLFASRIKIRKKQF 235
DB 181 RTCDAPFTYTGCGNDNNFVSRDECKRACAKALKKKKKMPKJLFASRIKIRKKQF 235

RESULT 2

ID AAB76856 standard; protein, 235 AA.

AC AAB76856;
DT 12-APR-2001 (first entry)

DE Human lung tumour protein related protein sequence SEQ ID NO:332.

KM Human; lung cancer; lung tumour; lung tumour protein; gene therapy;
KM lung cancer antigen; lung tumour-specific antigen; diagnosis; vaccine;
KM cytoskeletal; antisense inhibition.

OS Homo sapiens.

PN MO200100828-A2.

PD 04-JAN-2001.

PF 30-JUN-2000; 2000WO-US018061.

PR 30-JUN-1999; 99US-00346492.

PR 15-OCT-1999; 99US-00419356.

PR 17-DEC-1999; 99US-00466867.

PR 30-DEC-1999; 99US-00476230.

PR 06-MAR-2000; 2000US-00519642.

PR 22-MAR-2000; 2000US-00533077.

PR 10-APR-2000; 2000US-00546259.

PR 27-APR-2000; 2000US-00560406.

PR 05-JUN-2000; 2000US-00589184.

PA (CORI-) CORIYA CORP.

PI Wang T, Bangur CS, Lodes MJ, Fanger GR, Vedvick TS, Carter D;
PI Retter MW, Mannion J;

XX WPI: 2001-071488/08.

XX Example 1; Page 260-261; 436pp; English.

CC The present invention describes immunogenic portions of lung tumour-
CC associated proteins (I) and the nucleic acids (NAs) that encode them. (I)
CC have cytotoxic activity and can be used in gene therapy, antisense
CC inhibition and in vaccines. The NAs and the lung tumour-associated
CC proteins they encode may be used in the prevention, treatment and
CC diagnosis of diseases associated with their inappropriate expression,
CC especially lung cancers. For example, the NAs may be administered to
CC treat diseases by rectifying mutations or deletions in a patient's genome
CC that affect the activity of the protein by expressing inactive proteins

CC or to supplement the patients own production of (I). Additionally, the
CC NAs may be used to produce the lung-tumour associated protein, according
CC to standard recombinant DNA methodology. Conversely, antisense NA
CC molecules may be administered to down regulate protein expression by
CC binding with the cells own genes and preventing their expression. The NA
CC and complementary sequences may also be used as DNA probes in diagnostic
CC assays to detect and quantitate the presence of similar NA sequences in
CC samples, and hence which patients may be in need of treatment for lung
CC cancer. The (I) may be used as antigens in the production of antibodies
CC and in assays to identify modulators (agonists and antagonists) of the
CC expression and activity of the protein. AAF68083 to AAF68878 and AAB76848
CC to AAB76878 represent human lung tumour protein related nucleotide and
CC protein sequences which are used in the exemplification of the present
CC invention

XX Sequence 235 AA;

QY Query Match 100.0%; Score 1306; DB 4; Length 235;

Best Local Similarity 100.0%; Pred. No. 3.9e-114;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDPARPLGSLTLLFLTEALGDAAOEPTGNNNAEICLLPLDYGPCRALLLRYYDRYQS 60

DB 1 MDPARPLGSLTLLFLTEALGDAAOEPTGNNNAEICLLPLDYGPCRALLLRYYDRYQS 60

QY 61 CROFLYGCGEGNANNFYTWEACDDACWRIEKPVKYCRLOVSVDQCEGSTEKYPFNLSM 120

DB 61 CROFLYGCGEGNANNFYTWEACDDACWRIEKPVKYCRLOVSVDQCEGSTEKYPFNLSM 120

QY 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKIPSPFCYSPKDEGLCSANTVRYFNPXY 180

DB 121 TCEKFFSGGCHNRRIENRFPDEATCMGFCAPKIPSPFCYSPKDEGLCSANTVRYFNPXY 180

QY 181 RTCDAPFTYTGCGNDNNFVSRDECKRACAKALKKKKKMPKJLFASRIKIRKKQF 235

DB 181 RTCDAPFTYTGCGNDNNFVSRDECKRACAKALKKKKKMPKJLFASRIKIRKKQF 235

RESULT 3

ID AABG6429 standard; protein, 235 AA.

AC AABG6429;

DT 11-DEC-2002 (first entry)

DE Human ovarian cancer marker M588.

KM Human; ovarian cancer; marker; cancer; familial history; brain disorder;
KM central nervous system disorder; bacterial meningitis; viral meningitis;
KM Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus;
KM brain herniation; inflammation; encephalitis; testicular disorder;
KM nontuberculous granulomatous orchitis; connective tissue disorder;
KM heart disorder; ischemic heart disease; atherosclerosis; neoplasm;
KM histological type; carcinogenic; ovarian cancer marker.

OS Homo sapiens.

PN WO200271928-A2.

PD 19-SEP-2002.

PF 14-MAR-2002; 2002WO-US007826.

PR 14-MAR-2001; 2001US-0276025P.

PR 14-MAR-2001; 2001US-0276026P.

PR 10-AUG-2001; 2001US-0311732P.

PR 19-SEP-2001; 2001US-0323580P.

PR 26-SEP-2001; 2001US-0325102P.

PR 26-SEP-2001; 2001US-0325149P.

PR 26-SEP-2001; 2001US-0325149P.

XX (MILL-) MILLENNIUM PHARM INC.

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OM protein - protein search, using SW model

Run on: September 22, 2005, 10:02:10 ; Search time 43 Seconds
(without alignments)
407.966 Million cell updates/sec

Title: US-10-680-684-2
Perfect score: 1306
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
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4: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCOTS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	1306	100.0	235	1	US-08-147-710-2
4	1306	100.0	235	1	US-08-147-710-2
5	1306	100.0	235	1	US-08-147-710-2
6	1306	100.0	235	1	US-08-147-710-2
7	1306	100.0	235	1	US-08-147-710-2
8	1306	100.0	235	1	US-08-147-710-2
9	1306	100.0	235	1	US-08-147-710-2
10	1306	100.0	235	1	US-08-147-710-2
11	1306	100.0	235	1	US-08-147-710-2
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14	1306	100.0	235	1	US-08-147-710-2
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18	1306	100.0	235	1	US-08-147-710-2
19	1306	100.0	235	1	US-08-147-710-2
20	1306	100.0	235	1	US-08-147-710-2
21	1306	100.0	235	1	US-08-147-710-2
22	1306	100.0	235	1	US-08-147-710-2
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24	1306	100.0	235	1	US-08-147-710-2
25	1306	100.0	235	1	US-08-147-710-2
26	1306	100.0	235	1	US-08-147-710-2
27	1306	100.0	235	1	US-08-147-710-2

28	388	29.7	304	4	US-09-054-272-16	Sequence 16, Appl
29	388	29.7	304	6	5466783-2	Patent No. 5466783
30	388	29.7	304	6	5466783-2	Patent No. 5466783
31	388	29.7	304	6	5466783-2	Patent No. 5466783
32	388	29.7	304	6	5466783-2	Patent No. 5466783
33	388	29.7	304	6	5466783-2	Patent No. 5466783
34	388	29.7	304	6	5466783-2	Patent No. 5466783
35	388	29.7	304	6	5466783-2	Patent No. 5466783
36	388	29.7	304	6	5466783-2	Patent No. 5466783
37	388	29.7	304	6	5466783-2	Patent No. 5466783
38	388	29.7	304	6	5466783-2	Patent No. 5466783
39	388	29.7	304	6	5466783-2	Patent No. 5466783
40	388	29.7	304	6	5466783-2	Patent No. 5466783
41	388	29.7	304	6	5466783-2	Patent No. 5466783
42	388	29.7	304	6	5466783-2	Patent No. 5466783
43	388	29.7	304	6	5466783-2	Patent No. 5466783
44	388	29.7	304	6	5466783-2	Patent No. 5466783
45	388	29.7	304	6	5466783-2	Patent No. 5466783

ALIGNMENTS

RESULT 1
US-08-147-710-2
Sequence 2, Application US/08147710

Patent No. 5455338

GENERAL INFORMATION:

APPLICANT: Sprecher, Cindy A.

APPLICANT: Kistner, Walter

APPLICANT: Foster, Donald C.

TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND

NUMBER OF INVENTION: METHODS RELATING THERETO

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESS: ZymoGenetics, Inc.

STREET: 4225 Roosevelt Way, N.E.

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08147, 710

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Parker, Gary E

REGISTRATION NUMBER: 31-684

REFERENCE/DOCKET NUMBER: 93-14

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-547-8080 ext 322

TELEFAX: 206-548-2329

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 235 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-147-710-2

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Best Local Similarity 100.0%; Pred. No. 1.2e-123;

Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1-MDPARPLGSLILFLTEAAGDAQEPGNNATCFLPLVGPGRALLRYRYRYS 60

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Db 61 CROFLYGGCEGNANFFYWEACDCAWRIEKPVCRLQVSDVDCGSGSTKRYFENLSM 120
Qy 121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKTIPTSCYSPKDGCLGSANVTRYFENPRY 180
Db 121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKTIPTSCYSPKDGCLGSANVTRYFENPRY 180
Qy 181 RTCDAFYTYGGGNDNNFVSREDCKRACAKALKKKKKMPKLRFAIRIRKIRKQF 235
Db 181 RTCDAFYTYGGGNDNNFVSREDCKRACAKALKKKKKMPKLRFAIRIRKIRKQF 235

RESULT 2
US-08-458-090-2
; Sequence 2, Application US/08458090
; Patent No. 5728674
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Kistiel, Walter
; APPLICANT: Foster, Donald C.
; TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND
; TITLE OF INVENTION: METHODS RELATING THERETO
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,090
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31-648
; REFERENCE/DOCKET NUMBER: 93-14D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-090-2

Query Match 100.0%; Score 1306; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.2e-123;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 RTCDAFYTYGGGNDNNFVSREDCKRACAKALKKKKKMPKLRFAIRIRKIRKQF 235

RESULT 3
US-08-457-887-2
; Sequence 2, Application US/08457887
; Patent No. 5914315
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Kistiel, Walter
; APPLICANT: Foster, Donald C.
; TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS AND
; TITLE OF INVENTION: METHODS RELATING THERETO
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,887
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31-648
; REFERENCE/DOCKET NUMBER: 93-14D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-457-887-2

Query Match 100.0%; Score 1306; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 1.2e-123;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CROFLYGGCEGNANFFYWEACDCAWRIEKPVCRLQVSDVDCGSGSTKRYFENLSM 120
Db 61 CROFLYGGCEGNANFFYWEACDCAWRIEKPVCRLQVSDVDCGSGSTKRYFENLSM 120
Qy 121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKTIPTSCYSPKDGCLGSANVTRYFENPRY 180
Db 121 TCEKFFSGGCHRNRIENRFPDEATCMGFCAPKTIPTSCYSPKDGCLGSANVTRYFENPRY 180
Qy 181 RTCDAFYTYGGGNDNNFVSREDCKRACAKALKKKKKMPKLRFAIRIRKIRKQF 235
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RESULT 4
US-08-817-145-3
; Sequence 3, Application US/08817145
; Patent No. 6025329
; GENERAL INFORMATION:
; APPLICANT: Utsuno, Jun
; APPLICANT: SUDO, Tetsuo

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 22, 2005, 10:14:10 ; Search time 169 Seconds
(without alignments)
565.964 Million cell updates/sec

Title: US-10-680-684-2
Sequence score: 1306
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Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 1826521 seqs, 407012169 residues

Total number of hits satisfying chosen parameters: 1826521

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCIT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCITUS_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1306	100.0	235	US-09-904-621-2	Sequence 2, Appl1
2	1306	100.0	235	US-09-736-457-332	Sequence 332, App
3	1306	100.0	235	US-09-902-941-332	Sequence 332, App
4	1306	100.0	235	US-09-849-626-332	Sequence 332, App
5	1306	100.0	235	US-09-476-300-332	Sequence 332, App
6	1306	100.0	235	US-10-017-754-332	Sequence 332, App
7	1306	100.0	235	US-10-060-036-167	Sequence 316, App
8	1306	100.0	235	US-10-097-340-316	Sequence 316, App
9	1306	100.0	235	US-10-021-660-119	Sequence 119, App
10	1306	100.0	235	US-10-113-872-332	Sequence 332, App
11	1306	100.0	235	US-10-283-017-332	Sequence 332, App

12	1306	100.0	235	US-10-295-027-24	Sequence 24, Appl
13	1306	100.0	235	US-10-428-487-7	Sequence 7, Appl1
14	1306	100.0	235	US-10-211-462-52	Sequence 52, Appl1
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16	1306	100.0	235	US-10-800-057-2	Sequence 2, Appl1
17	1306	100.0	235	US-10-991-321-24	Sequence 24, Appl1
18	1200	91.9	213	US-09-766-778-2	Sequence 2, Appl1
19	1200	91.9	213	US-10-086-176A-6	Sequence 6, Appl1
20	703.5	53.9	184	US-10-425-115-318379	Sequence 318379,
21	464	35.5	88	US-09-978-418-26	Sequence 26, Appl
22	464	35.5	88	US-10-485-231-26	Sequence 26, Appl
23	394.5	30.2	291	US-09-992-600A-48	Sequence 48, Appl
24	394.5	30.2	291	US-09-924-340-48	Sequence 48, Appl
25	394.5	30.2	291	US-09-992-095B-48	Sequence 48, Appl
26	394.5	30.2	291	US-09-999-570-48	Sequence 48, Appl
27	394.5	30.2	291	US-10-000-489-48	Sequence 48, Appl
28	394.5	30.2	291	US-10-000-986-48	Sequence 48, Appl
29	394.5	30.2	291	US-10-154-678-48	Sequence 48, Appl
30	394.5	30.2	291	US-10-838-854-48	Sequence 48, Appl
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34	393.5	30.1	291	US-09-999-570-52	Sequence 52, Appl
35	393.5	30.1	291	US-10-000-489-52	Sequence 52, Appl
36	393.5	30.1	291	US-10-000-986-52	Sequence 52, Appl
37	393.5	30.1	291	US-10-154-678-52	Sequence 52, Appl
38	393.5	30.1	291	US-10-838-854-52	Sequence 52, Appl
39	388	29.7	304	US-10-167-351-1	Sequence 1, Appl1
40	388	29.7	304	US-10-167-351-1	Sequence 1, Appl1
41	388	29.7	304	US-10-755-544-3	Sequence 412, App
42	388	29.7	304	US-10-753-544-3	Sequence 3, Appl1
43	388	29.7	304	US-10-931-153-1	Sequence 1, Appl1
44	388	29.7	304	US-10-367-057-69	Sequence 69, Appl
45	388	29.7	304	US-10-953-902A-34	Sequence 54, Appl
			20	US-11-083-742-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-904-621-2
Sequence 2, Application US/0904621
Patent No. US20020098560A1
GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
APPLICANT: Kistel, Walter
TITLE OF INVENTION: NOVEL HUMAN KUNITZ-TYPE INHIBITORS
TITLE OF INVENTION: AND
FILE REFERENCE: 93-14D3
CURRENT APPLICATION NUMBER: US/09/904,621
PRIOR APPLICATION NUMBER: 2001-07-13
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 09/265,627
PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-09
PRIOR FILING DATE: EARLIER APPLICATION NUMBER: 5,455,338
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 235
TYPE: PRT
ORGANISM: Homo sapiens
US-09-904-621-2

Query Match 100.0%; Score 1306; DB 9; Length 235;
Best Local Similarity 100.0%; Pred. No. 2.6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MDPARPLGSLILFLTEAALGDAOEPTGNNAEICLLPDPYPCRALTLRYYYDRYTQS 60
1 MDPARPLGSLILFLTEAALGDAOEPTGNNAEICLLPDPYPCRALTLRYYYDRYTQS 60

Oy	6	CROELVGGCGNANNFPTWBAODCAWMRIEXKPKYCTLQVSVDQCCESTKEYPFNISM	120
Db	61	CROPFLVGCGGNANFYTWBAODCAWMRIEXKPKYCTLQVSVDQCCESTKEYPFNISM	120
Oy	121	TCEKFESGCGHRRRIENRFPDEATCMGFCAPKPISPCSPYDSEGLSANTRYTFENPRY	180
Db	121	TCEKFESGCGHRRRIENRFPDEATCMGFCAPKPISPCSPYDSEGLSANTRYTFENPRY	180
Oy	181	RTCDAFYYTCGGNDNNNFVSRSDCKRAKAKALAKKKKKPKLRFASRIIRIKTKQF	235
Db	181	RTCDAFYYTCGGNDNNNFVSRSDCKRAKAKALAKKKKKPKLRFSRIIRIKTKQF	235

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RESULT 2
US-09-736-457-332
Sequence 332, Application US/09736457
Patent No. US20020168637A1
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSeq For Windows Version 3.0
SEQ ID NO 332
LENGTH: 235
TYPE: PRM
ORGANISM: Homo sapiens
US-09-736-457-332

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Query Match	100.0%	Score 1306	DB 9	Length 235
Best Local Similarity	100.0%	Pred. No. 2.6e-116		
Matches	235	Conservative	0	Mismatches 0; Indels 0; Gaps 0
QY	1	MDPARPLGLSILLFLTEALGDAAOBETGNNAEILCLPLDYGPCRALLRYYDYRYQS	60	
Db	1	MDPARPLGLSILLFLTEALGDAAOBETGNNAEILCLPLDYGPCRALLRYYDYRYQS	60	
QY	61	CROFLYGGCEGNANNFYWEACDDACWFLIKYPKYCRQVSYDDCCBSTETKYPFNLSM	120	
Db	61	CROFLYGGCEGNANNFYWEACDDACWFLIKYPKYCRQVSYDDCCBSTETKYPFNLSM	120	
QY	121	TCEKFFSGGCHRRNIENRFPDEATCMGFCAPPKYISFCYSPDEGLCSANTVRYFENBRY	180	
Db	121	TCEKFFSGGCHRRNIENRFPDEATCMGFCAPPKYISFCYSPDEGLCSANTVRYFENBRY	180	
QY	181	RTCAFAFTYTGCGDNNVSRBDCGRACAKALKKKKKMPKLPFASRIRIKRKQF	235	
Db	181	RTCAFAFTYTGCGDNNVSRBDCGRACAKALKKKKKMPKLPFASRIRIKRKQF	235	

RESULT 3
US-09-902-941-332
Sequence 332, Application US/09902941
Patent No. US20020172952A1
GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Wang, Tongtong
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Rietter, Marc-W.
APPLICANT: Mameretakis, Margarita

```

: APPLICANT: Carter, Darick
: APPLICANT: Fanger, Gary R.
: APPLICANT: Vedrick, Thomas S.
: APPLICANT: Bangur, Chantalaya S.
: APPLICANT: Mcnabb, Andria
: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
: TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
: FILE REFERENCE: 210121.478C17
: CURRENT APPLICATION NUMBER: US/09/902,941
: CURRENT FILING DATE: 2001-07-10
: NUMBER OF SEQ ID NOS: 2002
: SOFTWARE: PatSeq for Windows Version 4.0
: SEQ ID NO 332
: LENGTH: 235
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-902-941-332

Query Match: 100.0%; Score 1306; DB 9; Length 235;
Query Local Similarity 100.0%; Pred. No.2.6e-116;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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QY	1	MDPARPGLSTLLFLFTEAALGDAAPGPTGNNAICLLPDIYGCRAALLKRYYYDRYQS	60
Db	1	MDPARPGLSTLLFLFTEAALGDAAPGPTGNNAICLLPDIYGCRAALLKRYYYDRYQS	60
QY	61	CRQPLVYGCCEGNANFPYTWEACDCAWRIEKVPKYLQVSVDDQCEGSTEKYEFFNLSSM	120
Db	61	CRQPLVYGCCEGNANFPYTWEACDCAWRIEKVPKYLQVSVDDQCEGSTEKYEFFNLSSM	120
QY	121	TCEKPFSGGCHRNRIENRFPDEATCMGFCAPKKIIPSCYSPKXDEGLCSANTRYENRY	180
Db	121	TCEKPFSGGCHRNRIENRFPDEATCMGFCAPKKIIPSCYSPKXDEGLCSANTRYENRY	180
QY	181	RTCDAPFYTGGCGDNNFVSRDCKRACAVALKKKKKKMPTKLRASRIKTIKKQF	235
Db	181	RTCDAPFYTGGCGDNNFVSRDCKRACAVALKKKKKKMPTKLRASRIKTIKKQF	235

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, RESULT 4
, US-09-849-626-332
, Sequence 332, Application US/09849626
, Publication No. US20020197669A1
, GENERAL INFORMATION:
, APPLICANT: Bangur, Chaitanya
, APPLICANT: Fangur, Gary
, APPLICANT: Wang, Aijun
, APPLICANT: Wang, Tongtong
, APPLICANT: Switzer, Anne
, APPLICANT: McNeill, Patricia
, APPLICANT: Clapper, Jonathan
, TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
, TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
, FILE REFERENCE: 210121.478C16
, CURRENT APPLICATION NUMBER: US/09/849,626
, CURRENT FILING DATE: 2001-05-03
, NUMBER OF SEQ ID NOS: 1926
, SOFTWARE: FastSeq for Windows Version 3.0
, SEQ ID NO 332
, LENGTH: 235
, TYPE: PR1
, ORGANISM: Homo sapiens
, US-09-849-626-332

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Qy	1	MDPARRPGSLTLLFLTEALGDAQOEPSTNNAETCLPLDYGSCRLALLRYDYDRYOS	60							
Dh	1	MDPARRPGSLTLLFLTEALGDAQOEPSTNNAETCLPLDYGSCRLALLRYDYDRYOS	60							
Qy	61	CROFLYGGSCGNANFNFTWEACDACMRIRKVPFVCLQVSVDDQCGSTTEKYFENLSM	120							

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: September 22, 2005, 09:59:56 / Search time 41 Seconds
(without alignments)
551.466 Million cell updates/sec

Title: US-10-680-684-2

Perfect score: 1306

Sequence: 1 MDPARPLGSHLLFLTEA.....KMPPLRPSAIRKIRKQF 235

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1306	100.0	235	2 A54951	tissue factor path
2	390	29.9	229	2 I46937	tissue factor path
3	388	29.7	304	1 TIHUGK	tissue factor path
4	384.5	29.4	304	1 JC2264	tissue factor path
5	376	28.8	302	1 TIRTKK	tissue factor path
6	372.5	28.5	300	2 S12143	lipoprotein-associ
7	366.5	26.5	306	2 S53325	tissue factor path
8	305.5	23.4	2225	2 T26063	hypothetical prote
9	303	23.2	2167	2 T34395	hypothetical prote
10	299	22.9	1965	2 T33216	hypothetical prote
11	292.5	22.4	1558	2 C89114	protein C37C3.6a.1
12	285	21.8	922	2 T23573	hypothetical prote
13	279.5	21.4	1522	2 H88380	protein T22F7.3 [i
14	271.5	20.8	1416	2 E88550	protein ZC84.1 [lm
15	271.5	20.8	2844	2 D88550	protein ZC84.6 [lm
16	268	20.5	1474	2 D88550	protein ZC84.6 [lm
17	268	20.5	1599	2 T16210	hypothetical prote
18	253.5	19.4	1043	2 T19734	hypothetical prote
19	252	19.3	1743	2 T26859	hypothetical prote
20	240	18.4	1391	2 T20406	hypothetical prote
21	239	18.3	838	2 T20125	hypothetical prote
22	215	16.5	252	2 JG0185	hepatocyte growth
23	215	16.5	1208	2 T27822	hypothetical prote
24	214	16.4	352	1 T1BOBI	alpha-1-microglobu
25	206	15.8	1203	2 T21275	hypothetical prote
26	199	15.2	692	2 T32960	hypothetical prote
27	197	15.1	228	2 T20219	hypothetical prote
28	196	15.0	123	2 A29652	inter-alpha-trypsi
29	191	14.6	337	1 T1PGBI	alpha-1-microglobu

30	188	14.4	183	2 T28711	hypothetical prote
31	186	14.2	125	1 T1BOBI	alpha-1-microglobu
32	186	14.2	349	2 S21089	alpha-1-microglobu
33	184.5	14.1	359	2 S35708	gamma-1-microglobu
34	182.5	14.0	355	1 S22181	alpha-1-microglobu
35	180	13.8	352	1 HCHU	hypothetical prote
36	178.5	13.7	502	2 T20130	hypothetical prote
37	174	13.3	61	1 T1VTR1	venom basic prote
38	173	13.2	335	2 T32657	hypothetical prote
39	172	13.2	62	2 S19327	venom basic prote
40	168	12.9	62	2 S07451	proteinase inhibit
41	166.5	12.7	372	2 JC2556	alpha-1-microglobu
42	165.5	12.7	110	1 T1TVOR	basic proteinase i
43	165	12.6	65	1 T1VIVC	venom basic protei
44	164	12.6	265	2 A53390	Kunitz-type protei
45	163	12.5	57	2 A59204	basic proteinase 1

ALIGNMENTS

10-11/1993

RESULT 1

tissue factor pathway inhibitor-2 precursor - human

N.Alternate names: placental protein 5 (PP5)

C.Species: Homo sapiens (man)

C.Date: 31-May-1996 #sequence revision 31-May-1996 #text change 09-Jul-2004

C.Accession: A54951; I55185; A34029; C34029; B34029

R.Sprecher, C.A.; Kistiel, W.; Mathewes, S.; Foster, D.C.

Proc. Natl. Acad. Sci. U.S.A. 91, 3353-3357, 1994

A>Title: Molecular cloning, expression, and partial characterization of a second human

A.Reference number: A54951; MUID:94211862; PMID:8159751

A.Accession: A54951

A.Status: translated from GB/EMBL/DBJ

A.Molecule type: mRNA

A.Residues: 1-235 <RES>

A.Cross-references: UNIPROT:P48307; GB:L27624; NID:G441149; PIDN:AAA20094.1; PID:G44115

A.Note: parts of this sequence, including the amino end of the mature protein, were det

A.Experimental source: Placenta

R.Miyagi, Y.; Koshikawa, N.; Yasumitsu, H.; Miyagi, E.; Hirahara, F.; Aoki, I.; Misugi,

J. Biochem. 116, 939-942, 1994

A>Title: cDNA cloning and mRNA expression of a serine proteinase inhibitor secreted by

A.Reference number: I55185; MUID:95204397; PMID:7896752

A.Accession: I55185

A.Status: nucleic acid sequence not shown; translation not shown; translated from GB/EN

A.Molecule type: mRNA

A.Residues: 1-235 <RES>

A.Cross-references: GB:D29992; NID:G484050; PIDN:BA06272.1; PID:G484051

A.Note: parts of this sequence, including the amino end of the mature protein, were det

R.Buetzow, R.; Huhntala, M.L.; Bohn, H.; Virtanen, I.; Seppälä, M.

Biochem. Biophys. Res. Commun. 150, 483-490, 1988

A>Title: Purification and characterization of placental protein 5.

A.Reference number: A34029; MUID:88106628; PMID:3276312

A.Accession: A34029

A.Molecule type: Protein

A.Residues: 'A', 24-33, 'X', 35 <BUE>

A.Accession: C34029

A.Molecule type: Protein

A.Residues: 47-50, 'X', 52-53 <BU2>

A.Accession: B34029

A.Molecule type: Protein

A.Residues: 133, 'X', 135-137, 'X', 139-140, 'X', 142-144, 'X', 146 <BU3>

A.Accession: 133, 'X', 135-137, 'X', 139-140, 'X', 142-144, 'X', 146 <BU3>

A.Molecule type: Protein

A.Residues: 133, 'X', 135-137, 'X', 139-140, 'X', 142-144, 'X', 146 <BU3>

A.Accession: 133, 'X', 135-137, 'X', 139-140, 'X', 142-144, 'X', 146 <BU3>

A.Molecule type: Protein

A.Residues: 133, 'X', 135-137, 'X', 139-140, 'X', 142-144, 'X', 146 <BU3>

A.Accession: 133, 'X', 135-137, 'X', 139-140, 'X', 142-144, 'X', 146 <BU3>

A.Molecule type: Protein

A.Residues: 133, 'X', 135-137, 'X', 139-140, 'X', 142-144, 'X', 146 <BU3>

A.Accession: 133, 'X', 135-137, 'X', 139-140, 'X', 142-144, 'X', 146 <BU3>

A.Molecule type: Protein

A.Residues: 133, 'X', 135-137, 'X', 139-140, 'X', 142-144, 'X', 146 <BU3>

A.Accession: 133, 'X', 135-137, 'X', 139-140, 'X', 142-144, 'X', 146 <BU3>

Query Match 100.0%; Score 1306; DB 2; Length 235;
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QY 1 MDPRPGLSLILLFLTEALGDAAEPTGNNABICLPDLYGFCRALLRYYDRYTG 60
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 QY 61 CROFLYGGCEGNANFYWEACDCAWRIEKVPVCRLOVSDQCGSTGEKYEFINSSM 120
 DB 61 CROFLYGGCEGNANFYWEACDCAWRIEKVPVCRLOVSDQCGSTGEKYEFINSSM 120
 QY 61 CROFLYGGCEGNANFYWEACDCAWRIEKVPVCRLOVSDQCGSTGEKYEFINSSM 120
 DB 61 CROFLYGGCEGNANFYWEACDCAWRIEKVPVCRLOVSDQCGSTGEKYEFINSSM 120
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 DB 121 TCERFSGGCHRNRIENRFPDEATCMGFCAPKCI PSFCYSPKDEGLCSANVTRYENPRY 180
 QY 121 TCERFSGGCHRNRIENRFPDEATCMGFCAPKCI PSFCYSPKDEGLCSANVTRYENPRY 180
 DB 121 TCERFSGGCHRNRIENRFPDEATCMGFCAPKCI PSFCYSPKDEGLCSANVTRYENPRY 180
 QY 181 RTCDAFYTTGGGNDNNFVSREDCRACAKLKKKKKPKLRPSRIKRIKKOP 235
 DB 181 RTCDAFYTTGGGNDNNFVSREDCRACAKLKKKKKPKLRPSRIKRIKKOP 235
 QY 181 RTCDAFYTTGGGNDNNFVSREDCRACAKLKKKKKPKLRPSRIKRIKKOP 235
 DB 181 RTCDAFYTTGGGNDNNFVSREDCRACAKLKKKKKPKLRPSRIKRIKKOP 235

RESULT 2
 146937
 tissue factor pathway inhibitor - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
 C/Accession: I46937
 R:Belasouni, A.; Kumpusamy, M.N.; Birktoft, J.J.; Bajaj, S.P.
 Thromb. Res. 69, 547-553, 1993
 A/Title: Revised cDNA sequence of rabbit tissue factor pathway inhibitor.
 A/Reference number: I46937; MUID:93276427; PMID:8503123
 A/Accession: I46937
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-299 <BEL>
 A/Cross-references: UNIPROT:P19761; GB:S61902; NID:G386015; PIDN:AA826836.1; PID:G386016
 C/Superfamily: tissue factor pathway inhibitor; animal Kunitz-type proteinase inhibitor
 F:49-99/Domain: animal Kunitz-type proteinase inhibitor homology <BFI1>
 F:120-170/Domain: animal Kunitz-type proteinase inhibitor homology <BFI2>
 F:212-262/Domain: animal Kunitz-type proteinase inhibitor homology <BFI2>

Query Match 29.9%; Score 390; DB 2; Length 299;
 Best Local Similarity 30.8%; Pred. No. 2e-27;
 Matches 88; Conservative 30; Mismatches 78; Indels 90; Gaps 7;

QY 12 LLLFLTEALGDAAEPTGNNABICLPDLYGFCRALLRYYDRYTG 59
 DB 13 LLLGLVPAPVSSAAEDEFNTIDIKPPLQKPTSHFCAMKVDGPRAYIKRFFPILTH 72
 QY 60 SCROFLYGGCEGNANFYWEACDCAWRIEKVPVCRLOVSDQCGSTGEKYEFINSSM 120
 DB 73 QCEERTYGGCEGNANFYWEACDCAWRIEKVPVCRLOVSDQCGSTGEKYEFINSSM 120
 QY 100 VSDQCGSTGEKYEFINSSMTCERFSGGCHRNRIENRFPDEATCMGFC----- 149
 DB 131 -----GYTRFYNNQSKQCEKFKYGGGLGLNL--NNEFSLSECKNTCENTPSDPOVD 180
 QY 150 -----APKTI---PSFCYSPKDEGLCSANVTRYENPRYRTCDAF 186
 DB 181 DHRDTQNTVNNNTLLINQPTKAPRPAWFGPSWCLPDPADGLCOANEIRFFVYALIGKCRPF 240
 QY 187 TYTGGGNDNNFVSREDCRACAKL-----KKKKMP 219
 DB 241 KYSGGGNDNNFVSREDCRACAKL-----KKKKMP 219

RESULT 3
 T1HUCK
 tissue factor pathway inhibitor precursor [validated] - human
 N/Alternate names: extrinsic pathway inhibitor; lipoprotein-associated coagulation inhib
 C/Species: Homo sapiens (man)
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C/Accession: A23712; A39176; A28650; A60433; B60433; S13034; A34315; A28294; S03903

R:Girard, T.J.; Eddy, R.; Wesselschmidt, R.L.; Macphail, L.A.; Likert, K.M.; Byers, M.G.
 J. Biol. Chem. 266, 5036-5041, 1991
 A/Title: Structure of the human lipoprotein-associated coagulation inhibitor gene. Intr
 A/Reference number: A23712; MUID:9161593; PMID:2002045
 A/Accession: A23712
 A/Molecule type: DNA
 A/Residues: 1-304 <GIR>
 A/Cross-references: UNIPROT:P10646; GB:M59493; GB:M59499; NID:G187204; PIDN:AA59526.1;
 Biochemistry 30, 1571-1577, 1991
 A/Title: Intron-exon organization of the human gene coding for the lipoprotein-associate
 A/Reference number: A39176; MUID:91129227; PMID:1993173
 A/Accession: A39176
 A/Molecule type: DNA
 A/Residues: 1-304 <VAN>
 A/Cross-references: GB:M58650; GB:J05312; NID:G186827; PIDN:AA59480.1; PID:G186829
 R:Wu, T.C.; Kretzmer, K.R.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.
 J. Biol. Chem. 263, 6001-6004, 1988
 A/Title: Cloning and characterization of a cDNA coding for the lipoprotein-associated cc
 A/Reference number: A28650; MUID:88198127; PMID:2452157
 A/Accession: A28650
 A/Molecule type: mRNA
 A/Residues: 1-304 <G12>
 A/Cross-references: GB:J03225; NID:G180545; PIDN:AA52022.1; PID:G180546
 A/Note: part of this sequence, including the amino end of the mature protein, was confir
 R:Girard, T.J.; Warren, L.A.; Novotny, W.F.; Bejcek, B.E.; Miletich, J.P.; Broze Jr., G.
 Thromb. Res. 55, 37-50, 1989
 A/Title: Identification of the 1.4 KB and 4.0 KB messages for the lipoprotein associated
 A/Reference number: A60433; MUID:89388722; PMID:2781520
 A/Accession: A60433
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-304 <G12>
 A/Experimental source: endothelial cells
 A/Accession: B60433
 A/Molecule type: protein
 A/Residues: 'XX', 31-53, 'X', 55-56 <G13>
 A/Experimental source: recombinant material from mouse C137 cells
 R:Girard, T.J.; McCourt, D.; Novotny, W.F.; Macphail, L.A.; Likert, K.M.; Broze Jr., G.J
 Biochem. J. 270, 621-625, 1990
 A/Title: Endogenous phosphorylation of the lipoprotein-associated coagulation inhibitor
 A/Reference number: S13034; MUID:91054349; PMID:2122883
 A/Accession: S13034
 A/Molecule type: protein
 A/Residues: 29-35 <G14>
 R:Novotny, W.F.; Girard, T.J.; Miletich, J.P.; Broze Jr., G.J.
 J. Biol. Chem. 264, 18832-18837, 1989
 A/Title: Purification and characterization of the lipoprotein-associated coagulation inh
 A/Reference number: A34315; MUID:90036996; PMID:2553722
 A/Accession: A34315
 A/Molecule type: protein
 A/Residues: 'XX', 31-33, 'L', 35-50 <NOV>
 A/Experimental source: plasma
 R:Pedersen, A.H.; Nordfang, O.; Norris, F.; Wiberg, F.C.; Christensen, P.M.; Moeller, K.
 J. Biol. Chem. 265, 16786-16793, 1990
 A/Title: Recombinant human extrinsic pathway inhibitor. Production, isolation, and chara
 A/Reference number: A28294; MUID:91009092; PMID:2211593
 A/Accession: A28294
 A/Molecule type: protein
 A/Residues: 29-41 <PED>
 R:Girard, T.J.; Warren, L.A.; Novotny, W.F.; Likert, K.M.; Brown, S.G.; Miletich, J.P.;
 Nature 338, 518-520, 1989
 A/Title: Functional significance of the Kunitz-type inhibitory domains of lipoprotein-as
 A/Reference number: S03903; MUID:89181950; PMID:2927510
 A/Contents: annotation; site-directed mutagenesis
 C/Comment: The first Kunitz-type domain binds the factor VIIa/tissue factor complex; the
 C/Genes: GDB:TFPI
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 A/Cross-references: GDB:127364; OMIM:152310
 A/Map position: 2q32-2q32
 A/Introns: 41/1; 107/1; 120/1; 179/1; 210/1; 270/1
 C/Function:
 A/Description: regulates clotting by factor Xa-dependent inhibition of the coagulation f

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 22, 2005, 09:36:09 ; Search time 172 Seconds
(without alignments)
699,643 Million cell updates/sec

Title: US-10-680-684-2

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1306	100.0	235	1 TFP2 HUMAN	P48307 homo sapien
2	1231.5	94.3	224	2 Q8NAK6	Q8NAK6 homo sapien
3	943.5	72.2	167	2 Q8NR89	Q8NR89 homo sapien
4	939.5	71.9	234	2 Q7YR08	Q7YR08 bos taurus
5	654	50.1	230	2 Q8CF99	Q8CF99 ratu
6	644	49.3	230	1 TFP2 MOUSE	Q35536 mus musculu
7	635	48.6	224	2 Q7T0Z5	Q7T0Z5 xenopus lae
8	388	29.7	304	1 TFP1 HUMAN	B10646 homo sapien
9	387.5	29.7	300	1 TFP1 RABIT	F19761 oryctolagus
10	387	29.6	287	2 Q93424	Q93424 cyprinus ca
11	384.5	29.4	304	1 TFP1 MACMU	Q28864 macaca mula
12	378	28.9	306	1 TFP1 MOUSE	Q54819 mus musculu
13	376	28.8	302	1 TFP1 RAT	Q02445 ratu
14	367.5	28.1	279	2 Q7Z4Z2	Q7Z4Z2 brachydanio
15	361	27.6	241	2 Q7PKX1	Q7PKX1 anopheles g
16	358.5	27.5	759	2 Q81T91	Q81T91 ancylostoma
17	357.5	27.4	3198	2 Q9U8G8	Q9U8G8 manduca sex
18	346.5	26.5	336	2 Q28874	Q28874 canis fami
19	336.5	25.8	2772	2 Q9VAV4	Q9VAV4 drosophila
20	336.5	25.8	2776	2 Q86940	Q86940 drosophila
21	336.5	25.8	2894	2 Q7KRX2	Q7KRX2 drosophila
22	336.5	25.8	2898	2 Q86829	Q86829 drosophila
23	325	24.9	1572	2 Q44938	Q44938 haemochus
24	310.5	23.8	2174	2 Q9G0R0	Q9G0R0 drosophila
25	305.5	23.4	2225	2 Q45861	Q45861 caenorhabdi
26	305	23.4	1487	2 Q8MPV5	Q8MPV5 caenorhabdi
27	303	23.2	2167	2 Q76840	Q76840 caenorhabdi
28	299	22.9	1949	2 Q8MXG3	Q8MXG3 caenorhabdi
29	292.5	22.4	1558	2 Q81710	Q81710 caenorhabdi
30	285	21.8	922	2 Q21418	Q21418 caenorhabdi
31	282	21.6	235	2 Q8BSB7	Q8BSB7 mus musculu

32	282	21.6	235	2 Q8CT80	Q8CT80 mus musculu
33	281	21.5	1666	2 Q8MXG2	Q8MXG2 caenorhabdi
34	279.5	21.4	988	2 Q22685	Q22685 caenorhabdi
35	276	21.1	277	2 Q8AYE1	Q8AYE1 brachydanio
36	272.5	20.9	327	2 Q6IND9	Q6IND9 xenopus lae
37	272	20.8	142	2 Q8WPI3	Q8WPI3 boophilus lae
38	271.5	20.8	1416	1 YN81 CAEEL	YN81 CAEEL
39	269.5	20.6	507	2 Q61750	Q61750 ratu
40	269	20.6	507	1 SPT1 MOUSE	SPT1 MOUSE
41	268	20.5	339	2 Q68G55	Q68G55 mus musculu
42	268	20.5	507	2 Q9D3K4	Q9D3K4 mus musculu
43	268	20.5	507	2 Q9J0I4	Q9J0I4 mus musculu
44	268	20.5	1474	2 Q62504	Q62504 caenorhabdi
45	268	20.5	1599	2 Q09983	Q09983 caenorhabdi

ALIGNMENTS

RESULT 1
TFP2 HUMAN
ID TFP2 HUMAN STANDARD; PRT; 235 AA.
AC P48307
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tissue factor pathway inhibitor 2 precursor (TFPI-2) (Placental
protein 5) (PP5).
GN Name=TFPI2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euteria; Primates; Carnivora; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=95204397; PubMed=7896752;
RA Miyagi Y., Koshikawa N., Yasumitsu H., Miyagi E., Hirahara F.,
Aoki I., Mitsu K., Umeda M., Miyazaki K.;
RT "CDNA cloning and mRNA expression of a serine proteinase inhibitor
secreted by cancer cells: identification as placental protein 5 and
tissue factor pathway inhibitor-2.";
RL J. Biochem. 116:939-942(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94211862; PubMed=8159751;
RA Sprecher C.A., Kistiel W., Mathews S., Foster D.C.;
RT "Molecular cloning, expression, and partial characterization of a
second human tissue-factor-pathway inhibitor.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:3353-3357(1994).
RN [3]
RP SEQUENCE FROM N.A.
RA Maggi L.;
RL Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grove L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
Diatchenko L., Murusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheltz T.E.,
Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosnak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gnanapane P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalske U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP PARTIAL SEQUENCE OF 23-35; 47-53 AND 133-146.
 RC TISSUE=Placenta;
 RX MEDLINE=88106628; PubMed=3276312;
 RA Buetzow R., Huhtala M.-L., Bohn H., Virtanen I., Seppälä M.,
 RT "Purification and characterization of placental protein 5.";
 RL Biochem. Biophys. Res. Commun. 150:483-490(1988).
 RP ERRATUM.
 RA Buetzow R., Huhtala M.-L., Bohn H., Virtanen I., Seppälä M.,
 RL Biochem. Biophys. Res. Commun. 151:630-631(1988).
 CC -1- FUNCTION: Seems to inhibit trypsin, factor VIIa/tissue factor,
 CC weakly factor Xa. Has no effect on thrombin.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Umbilical vein endothelial cells, liver,
 CC placenta, heart, pancreas, and maternal serum at advanced
 CC pregnancy.
 CC -1- DOMAIN: This inhibitor contains three inhibitory domains.
 CC -1- SIMILARITY: Contains 3 BPTI/Kunitz inhibitor domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D29992; BA06272.1; -;
 DR EMBL; L27624; AA020094.1; -;
 DR EMBL; AC002076; AA02022.1; -;
 DR EMBL; AF217542; AA03254.1; -;
 DR EMBL; BC005330; AA05330.1; -;
 DR PIR; A54951; A54951.
 DR HSSP; P10646; 11RH.
 DR Genew; HGNC:11761; TFP12.
 DR H-InVDB; HIX0006849; -;
 DR MIM; 600033; -;
 DR GO; GO:0005578; C:extracellular matrix; TAS.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; TAS.
 DR InterPro; IPR002223; Prot. Inh. Kunitz-m.
 DR InterPro; IPR008296; TFP1.
 DR Pfam; PF00014; Kunitz BPTI; 3.
 DR PIRSF; PIRSF01620; TFP1; 1.
 DR PRINTS; PR00759; BASICTPASE.
 DR PRODom; PD000222; Prot. Inh. Kunitz-m; 3.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 2.
 DR PROSITE; PS02079; BPTI_KUNITZ_2; 3.
 KW Blood coagulation; Direct protein sequencing; Glycoprotein;
 KW Polymorphism; Repeat; Serine protease inhibitor; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 235 Tissue factor pathway inhibitor 2.
 FT DOMAIN 36 86 BPTI/Kunitz inhibitor 1.
 FT DOMAIN 96 149 BPTI/Kunitz inhibitor 2.
 FT DOMAIN 158 208 BPTI/Kunitz inhibitor 3.
 FT DOMAIN 213 217 POLY-lys.
 FT SITE 46 47 Reactive bond (By similarity).
 FT SITE 107 108 Reactive bond (By similarity).
 FT SITE 168 169 Reactive bond (By similarity).
 FT DISULFID 36 86 By similarity.

FT DISULFID 45 69 By similarity.
 FT DISULFID 61 82 By similarity.
 FT DISULFID 96 149 By similarity.
 FT DISULFID 106 130 By similarity.
 FT DISULFID 122 145 By similarity.
 FT DISULFID 158 208 By similarity.
 FT DISULFID 167 191 By similarity.
 FT DISULFID 183 204 By similarity.
 FT CARBOHYD 116 116 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 170 170 N-linked (GlcNAc...) (potential).
 FT VARIANT 102 102 V -> A (in dbSNP:1804202).
 FT COMPACT 23 23 /FTID=VAR_012005.
 FT SEQ SEQUENCE 235 AA; 26934 MW; 975ABAS53F7C65F CRC64;
 Query Match 100.0%; Score 1306; DB 1; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1.2e-110; Indels 0; Gaps 0;
 Matches 235; Conservative 0; Mismatches 0;
 QY 1 MDPARPLGSLILLFTTEALGDAQEPYNNALICLPLDYGPCRALILRYRYRTQS 60
 DB 1 MDPARPLGSLILLFTTEALGDAQEPYNNALICLPLDYGPCRALILRYRYRTQS 60
 QY 61 CROFLYGCCEGNANFYWEACDDACWRIEKYPKVCRLQVSYDDQCEGSTEYFNLSSM 120
 DB 61 CROFLYGCCEGNANFYWEACDDACWRIEKYPKVCRLQVSYDDQCEGSTEYFNLSSM 120
 QY 121 TCCKFFSGGCHNRRLENRPDEATCWCPCAPKKIBFCFSPDEGLCSANTRYNPNRY 180
 DB 121 TCCKFFSGGCHNRRLENRPDEATCWCPCAPKKIBFCFSPDEGLCSANTRYNPNRY 180
 QY 181 RTCDATFYTGCGGNDNPFNSREDCKRACAKALKKKKPKLAFASIRIRIRKKOF 235
 DB 181 RTCDATFYTGCGGNDNPFNSREDCKRACAKALKKKKPKLAFASIRIRIRKKOF 235
 RESULT 2
 ID Q8NAK6 PRELIMINARY; PRT; 224 AA.
 AC Q8NAK6;
 DT 01-OCT-2002 (TEMBLrel). 22, Created)
 DT 01-OCT-2002 (TEMBLrel). 22, Last sequence update)
 DE Hypoetical protein FLJ35180.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Makanatu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Obaishi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
 RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira T., Kikawa E., Omura Y.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Niimura K., Iehibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimata M., Watanabe M., Hirake S., Chiba Y., Ishida S.,
 RA Ono Y., Takiguchi S., Watanabe M., Hosoda M., Hottu T., Kusano J.,
 RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hiroo M., Ohmori Y.,